Supplementary information, Data S1 Extended Experimental Procedures

Plasmids construction

Total RNAs were extracted from 293T or 3T3-L1 cells using Tri-reagent (Sigma). cDNA was synthesized by RevertAid First Strand cDNA Synthesis kit with random primers (Thermo). The human FTO (Gene ID: 79068) open reading frame encoding the full-length proteins were amplified and subcloned into pEGFP-C1B using the following primers: forward (Xho I): 5'-GATCTCGAGCTATGAAGCGCACCCCGACTGC-3', reverse (Kpn I): 5'-CGGGGTACCCTAGGGTTTTGCTTCCAGAA-3'. The mouse RUNX1T1 (Gene ID: 12395) were open reading frame encoding the full-length proteins were amplified and subcloned into pEGFP-C1B using the following primers: forward (Xho I): 5'-CCGCTCGAGATGCCTGATCGTACCGAGAAG-3', reverse (Not I): 5'-ATAAGAATGCGGCCGCCTAGCGAGGCGTCGTCTC-3'. The alternatively spliced isoform of mouse RUNX1T1 were generated and subcloned into pEGFP-C1B using the following primers: forward (Xho I): 5'-CCGCTCGAGATGCCTGATCGTACCGAGAAG-3', reverse (Not I): 5'-CCGGCGGCCGCTCAATCATTTCTTCTTGACGTGTGCCATGTAACC CTGTCTGGAGTTCGCCTCTTCC-3'. Human SR plasmids of proteins were bought from Origene (OriGene Technologies, Rockville, MD). The expression constructs were generated using PCR and subcloned into pCS2-Flag vectors with an N-terminal FLAG tag [3]. The human SRSF2 (Gene ID: 6427): forward (EcoR I): 5'-GGGGAATTCAGCTACGGCCGCCCCCC-3', reverse (Xho I): 5'-GGGCTCGAGTTAAGAGGACACCGCTCCTTCC-3'. The human SRSF4 (Gene ID: 6429): forward (EcoR I): 5'- GGGGAATTCCCGCGGGTGTACATCGG-3', reverse (Xho I): 5'-GGGCTCGAGTTAGGACCTTGAGTGGG-3'. Functional mutants of FTO were generated by PCR from pEGFP-C1B-FTO. Point mutations to generate the catalytic mutant pEGFP-C1B-FTO-HDH (H231A/D233A/H307A) were introduced using the Quik-change site-directed mutagenesis kit (Stratagene) with the following primers: 5'-GAAAATGGCAGTGAGCTGGGCTCATGCTGAAAATCTGGTGGACAGG-3' and 5'-CAATGCCACCCACCAAGCCTGTGTTTTGGCCGG-3'.

Cell culture and adipocyte differentiation

3T3-L1 pre-adipocytes were grown in DMEM Dulbecco's Modified Eagle Medium (DMEM) containing 10% newborn calf serum (NBCS) (SH30401.01, Hyclone) and 1% antibiotics until confluence and induced to differentiation similarly as previously described [4, 5]. Cells were seeded with 30% confluence (referred as D-2). After two days post-confluence (D0), cells were exposed to differentiation medium containing 0.5mmol/L isobutylmethylxanthine (I5879, Sigma), 1μmol/L dexamethasone (D2915, Sigma), 10μg/mL insulin (I6634, Sigma), 2μmol/L rosiglitazone (R2408, Sigma) and 10% fetal bovine serum (FBS) (A15-151, PAA) for three days (D3). At the end of day 3, culture medium was replaced with DMEM supplemented only with 10ug/mL insulin and 10% FBS, and replenished every other day. After the differentiation process, at least 90% of the cells had accumulated lipid droplets at day 10 (D10), and were used as mature adipocytes.

Oil red O staining

Maturation of adipocytes was confirmed by Oil Red O staining. It was performed as previously described with minor modifications [6]. Cells were rinsed twice in PBS prior to fixing with 10% paraformaldehyde for 1h at room temperature (R.T). After rinsing twice with PBS, cells were incubated in 60% (wt/wt) filtered Oil Red O Stock (0.6g of Oil Red O powder (O-0625, Sigma) in 100ml of isopropanol) with water (3:2) for one hour at room temperature. Then, the cells were washed twice with distilled water to remove excess dye and photographed under microscopy.

Triglyceride (TG) assay

Measurement of the intracellular TG content was performed as the manufacturer's protocol of the Tissue triglyceride assay kit (E1003-2, Applygen, China). Cells were collected by trypsinization and washed twice with PBS. After trashing the PBS, cells were lysed in the lysis buffer provided in the kit. After treated at 70 ℃ for 10min and centrifuged, the supernatant was incubated with R1:R2 mixture with the ratio of 4:1 at 37 ℃ for 10min. The absorbance value at 500nm which is proportional to the concentration of triglyceride was obtained with a spectrophotometer. Cells undergoing the same treatment conditions were lysed in RIPA buffer for protein concentration determination and data normalization.

Plasmid transfection and RNA interference

Mouse FTO siRNAs were designed and synthesized by Genepharma Corporation. The following siRNA were synthesized (GenePharma, China) and used in the study: FTO #1: 5'-GCAGCUGAAAUACCCUAAA-3', FTO #2: 5'-CAGGCACCUUGGAUUAUA-3', FTO #3: 5'-GGUGCUCCGUGAAGUUAAA-3'. ALKBH5 #1: 5'-ACAAGUACUUCUUCGGCGA-3', ALKBH5 #2: 5'-CUGAGAACUACUGGCGCAA-3', ALKBH5 #3: 5'-GCGCCGUCAUCAACGACUA-3'. METTL3 #1: 5'-GGAGAUCCUAGAGCUAUUA-3', METTL3 #2: 5'-CUGCACUUCAGACGAAUUA-3', METTL3 #3: 5'-GCUACCGUAUGGGAACAUUA-3'. SRSF2 #1: 5'-GAAGAAGAGGGAGCAGUU-3', SRSF2 #2: 5'- GCGCGTCTTCGAGAAATAC-3', SRSF2 #3: 5'-CCCGAAGAUCCAAGUCCAATT-3'. Scrambled siRNA (siCTRL): 5'-UUCUCCGAACGUGUCACGU-3'.

Transfections were performed with Lipofectamine RNAiMAX (Invitrogen) for siRNA, and Lipofectamine 2000 (Invitrogen) for plasmid transfection following the manufacturer's instructions. For FTO rescue experiments, cells were co-transfected with 1μg of plasmid DNA and 60pmol siRNA using Lipofectamine 2000.

Analysis of m^6A level using dot-blot assay

mRNAs were extracted using Dynabeads® mRNA Purification Kit (61006, Ambion) following the manufacturer's instruction. mRNAs were hybridized onto Amersham Hybond-N^+ membrane (GE Healthcare) by using Bio-Dot®Microfiltration Apparatus (170-6545，GE Healthcar) in two-fold serial dilutions. After UV crosslinking and baking at 80 ℃, the blotted membrane was washed by 1×PBST buffer, blocked with 5% of non-fat milk, and incubated with anti-m^6A antibody (1:2000; Synaptic Systems) overnight at 4 ℃. After incubating with horseradish peroxidase (HRP)-conjugated anti-rabbit IgG secondary antibody, the membrane was visualized by ECL Western Blotting Detection Kit (RNP2232, GE healthcare). To ensure

an equal amount of mRNA was spotted on the membrane, the same blot was stained with 0.02% methylene blue in 0.3M sodium acetate (pH 5.2).

Western blot analysis

Total protein lysate were extracted from 3T3-L1 cells with RIPA buffer. Protein concentrations were measured using the Bradford Assay, and 50-100μg protein extracts were subjected to SDS-PAGE. Then proteins were transferred to a nitrocellulose membrane, blocked with 5% non-fat milk and incubated with first antibodies for 1h at R.T. After incubation with secondary antibody against mouse (1:10,000) or rabbit (1: 10,000) for 1h at R.T, the membrane was visualized by ECL Western Blotting Detection Kit (RNP2232, GE healthcare).

RNA isolation, cDNA synthesis and semi-quantitative PCR

Total RNA was extracted using TRI® Reagent (Sigma). cDNA was synthesized by RevertAid™ First Strand cDNA Synthesis Kit with Oligo dT primers (K1622, Fermentas) following manufacturer's recommendations. PCR reactions were carried out on a DNAEngine® Thermal Cycler (PTC-0200G, Bio-Rad) in 25μl reaction volume containing 1μl cDNA, 200nM primer pairs and components of TaKaRa Taq™ kit (R001A, Takara). All samples were analyzed in triplicate RT-qPCR. The primer pairs used for detection of transcripts were used in the study: FTO (forward): 5'-AGGAAATCCATAATGAGG-3', FTO (reverse): 5'-TGAGGTCAAAGGGCAGAG-3'. METTL3 (forward): 5'-TGATTGAGGTAAAGCGAGGTC-3', METTL3 (reverse): 5'-TCCTGACTGACCTTCTTGCTC-3'. ADIPSIN (forward): 5'-GCACACTGCATGGATGGAGT-3', ADIPSIN (reverse): 5'-CTAGAGGGCTGCCGGAGTCT-3'. PREF-1 (forward): 5'-GGCAGTGCATCTGCAAGGAT-3', PREF-1 (reverse): 5'-GTTCTGGCACGGGCCACT-3'. ACTIN (forward): 5'-AGCCATGTACGTAGCCATCC-3', ACTIN (reverse): 5'-CTCTCAGCTGTGGTGGTGAA-3'. GKAP1 (forward): 5'-TGAGCTTTCATCGCCAAACC-3', GKAP1 (reverse): 5'-GTTTGTCCTTGCCCTGGTG-3'. ZFP809 (forward): 5'-ATTTGGAGCGTGGATTTGGG-3', ZFP809 (reverse): 5'-TTGGTTCTCTGTGACTTGCG-3'. FBXO9 (forward): 5'-CCGACCGAGAACTCTGCTAA-3', FBXO9 (reverse): 5'-CCTGGGGTCAGTTCAAACAT-3'. KIF13A (forward): 5'-GTGGGAAGAGAAGCTGAGGA-3', KIF13A (reverse): 5'-TCTTTGGGCGTGAGAGTGAT-3'. ZFP212 (forward): 5'-TGGCAGAAGGAGCTCTACAG-3', ZFP212 (reverse): 5'-AGAAAGCCTGCTGTTCAACTG-3'. Runx1t1 (forward): 5'-CAGCGTGAACTCCTCCACTG-3', Runx1t1 (reverse): 5'-CGAGATGTTTCCACTCTTCTG -3'

M^{6}A-seq

mRNAs were extracted using Dynabeads® mRNA Purification Kit (61006, Ambion) and were fragmented into 100nt length by using RNA Fragmentation Reagents (AM8740, Ambion). 4μg Fragmented mRNAs were denatured for 5min at 75℃ and were incubated for 3 h at 4℃ with 8μg of affinity purified anti-m^{6}A polyclonal antibody (202003, Synaptic Systems) in IPP

buffer (150mM NaCl, 0.1% NP-40, 10mM Tris-HCl, pH 7.4). The mixture was then subjected to immunoprecipitation by incubation with protein-A beads (P9424, Sigma-Aldrich) at 4℃ for overnight. After sufficient washing, bound RNA was eluted from the beads with 0.5 mg/ml N^6-methyladenosine (P3732, Berry & Associates) in IPP buffer, and ethanol precipitated. The eluted RNA was resuspended in H_2O and used to generate the cDNA library according to TruSeq RNA Sample Prep Kit protocol, which was then sequenced using the HiSeq 2000 system (Illumina) according to the manufacturer's instructions. [1, 2].

Alignment of seq-data

All samples were sequenced by Illumina Hiseq2000 with single end 101-bp read length. Raw RNA-seq reads for each sample were stripped of adaptor sequence with Cutadapt software (http://code.google.com/p/cutadapt/) and removed low quality bases using Trimmomatic [7]. Processed reads with length less than 20nt or contained an ambiguous nucleotide were discarded. The remained reads were mapped to the mouse reference genome version mm10 by Tophat version 2.0.4, without any gaps and allowed for at most two mismatches [8, 9].Unique mapped reads with mapping quality larger than or equal to 20 were kept for the subsequent analysis.

M^6A peaks identification

M^6A regions (m^6A peaks) were identified by comparing the read abundance between m^6A-seq and RNA-seq samples of the same loci with a method applied in previous report [1]. Briefly, the entire mm10 genome was divided into 25nt bins and the numbers of both m^6A-seq reads and RNA-seq reads (used as control) mapped to each bin were counted by BEDTools' intersectBed and compared [10]. Bins with statistically enriched m^6A-seq reads compared with the RNA-seq reads (adjusted *p* value <1e-5, Fisher's exact test together with Benjamini-Hocberg procedure) were identified and concatenated adjacently with BEDTools' mergeBed [10]. Concatenated m^6A-seq reads enrichment regions with length less than 75nt were filtered out. In some cases, the length of the concatenated windows spanned > 200nt, these windows were split into peaks between 200nt smaller peaks. Using the same selection criteria, regions with significantly enriched RNA-seq reads were selected as control peaks.

Annotation of m^6A peaks

M^6A peaks were mapped to the coding sequences (CDS), 5'UTRs, 3'UTRs and introns, in that order by using intersectBed from BEDTools according to the gene annotations (Ensembl version 68) [10]. Considering that individual m^6A peaks often mapped to multiple transcript variants of the same gene, only one transcript variant with the most exon numbers per gene was used here. Meanwhile, adjacent genes on the genome with overlapping transcripts were discarded to avoid mis-assignment of m^6A peaks. The peak annotations were then compiled into the pie chart distributions. The distribution for the original control data sets was computed in a similar fashion.

Motif analysis for m^6A peaks

Sequence motifs enriched in m^6A peaks were identified by HOMER [11], a suite of tools for motif discovery and next-generation sequencing analysis. In the analysis procedure, the m^6A peaks were set as the target sequences and control peaks as the background, with the parameter

for motif length from 5 to 8. Motifs only enriched among m^{6}A peaks (*p* value < 1e-10) were identified and plotted by Weblogo [12].

Differential expressed genes and isoforms

To the RNA-seq data, the number of reads mapped to each Ensembl gene (release 68) was counted using the HTSeq python package (http://www-huber.embl.de/users/anders/HTSeq/doc/overview.html), with the 'union' overlap resolution mode, and -stranded=no. The R-package DEGseq with the method MARS (MA-plot-based method with random sampling model) were used to determine the differentially expressed genes in different samples (*p* value cutoff = 0.001) [13]. Meanwhile, the expressions of transcripts were quantified as Reads Per Kilobase of exon model per Million mapped reads (RPKM).

Based on the TopHat2 results of RNA-seq data, Cuffdiff, as part of the Cufflinks package (version 2.0.2) [14] with –G parameter which means that quantification against reference transcript annotation were applied to calculated the reads count and FPKM (Fragments Per Kilobase of exon model per Million mapped reads) for each isoform of each gene. The reads count for each isoform were used as input for DEGseq to calculate the significant differentially expressed isoforms with the method MARS (*p* value cutoff = 0.001).

Relationship of m^{6}A enrichment and gene expression

The peak enrichment was computed for each peak by dividing the number of m^{6}A IP reads by the number of non-IP (control) reads that mapped to that peak, each normalized for the total number of reads that were mapped. This method allowed us to determine the relative frequency of methylation at a given m^{6}A peak region [1].

To all genes with m^{6}A peak, Pearson correlation coefficient of m^{6}A enrichment and gene's RPKM was calculated using the R package. To gene with multiple m^{6}A peaks, the average enrichment value was treated as the gene's whole m^{6}A enrichment.

Alternative splicing analysis

Scripture, one software for transcriptome reconstruction was used to detect 7 category splicing events (exon skipping (ES), alternative 5'ss and 3'ss selection (A5SS and A3SS), change of the first and last exon (CFE and CLE), alternative of the first and last exon (AFE and ALE)) occurred to each gene in the RNA-seq samples [15]. It can provide the whole isoform number and their exon constitution for each gene. To each isoform, its splicing events calculated by comparing the reference annotation were generated. In addition, if isoform number or constitution for one gene in one sample was different from that in the other RNA-seq sample, this gene may be with alternative splicing event.

Differentially expressed exons analysis was done by the R package DEXSeq [16]. The package provides a method to systematically detect differential exon usage. First, non-overlapping exonic regions for mm10 were defined using the 'dexseq_prepare_annotation.py' script provided as part of the DEXseq package. Next the number of reads falling in each of the defined exonic regions was counted using the DEXseq script 'dexseq_count.py' with parameters –a=20 to exclude multi-reads mapped to different locations of the genome, and –stranded=no. To differentially expressed introns analysis, the number of reads falling in each intron was counted using RSeQC, one software for quality control of RNA-seq experiments [17], and differential expression analysis was done using the

DEGseq [13].

Exon-exon junctions (EEJs) methods applied in previous study [18] was also used to analyze alternative splicing event. Information on intron-exon structures was extracted from Ensembl annotations (release 68) for mouse (mm10) genomes. From the resulting datasets, a Bowtie library of non-redundant EEJ sequences was generated for mouse by combining every possible (forward combination) of splicing donor and acceptor within each gene. The outputs were parsed to identify EEJs with continuous or discrete exon number, which means for constitutive or alternative splicing. If reads were aligned to EEJs with discrete exon number, it indicate that this gene has alternative splicing event in the sample.

Spatial correlation of m^{6}A modification and binding sites of SR protein

SRSF1 and SRSF2 CLIP-tag clusters were downloaded from starBase V2.0 [19]. Other SR protein CLIP-seq data were downloaded from SRA and the Array Express database. (http://www.ebi.ac.uk/arrayexpress/) and binding clusters of them were analyzed by CLIPper tool (https://github.com/YeoLab/clipper/wiki/CLIPper-Home) [20]. Motifs of these clusters were calculated by HOMER. The CLIP-tag clusters were set as the target sequences and the set of background clusters was generated with BEDTools' shuffleBed program to randomly shuffle regions of the same size as the CLIP-tag clusters throughout gene regions. Clusters distribution in the splice junctions were also analysed with above methods used to m^{6}A peak. Meanwhile, we used the BEDTools'closestBed to calculate the distance of SR proteins clusters and m^{6}A sites. Control clusters were generated with BEDTools' shuffleBed to randomly shuffle regions of the same size as the clusters. Meanwhile, the web-based program ESEfinder was employed to identify genomic locations with sequence motifs, acting as ESEs in response to SRSF1 and SRSF2, with highest score above threshold values according to the nucleotide frequency matrices. Then we used the BEDTools' closestBed to calculate the distance between four categories of ESEs recognized by above four SR proteins and m^{6}A sites, as well as RRACH sites. As control, randomly selected sites with same length as m^{6}A peaks and RRACH motif within the same exons were generated with BEDTools' shuffleBed. In all these analyses, the randomly selected background peaks were shuffled a total of 1000 times, and the average of the total number of overlaps or distances was used for the random counts. To regions with both m^{6}A peak and SR proteins binding, phylogenetic conservation of them was done by comparing PhyloP [21] scores of these overlapped regions to those same regions randomly shuffled within gene exons using BEDTools. PhyloP scores were computed using complete MOTIFs (http://cmotifs.tchlab.org/), which uses the phastCons scores from vertebrates. Significant differences in the distributions of the PhyloP scores were determined with the Kolmogorov-Smirnov (K-S) test in the R programming package.

Assignment of m^{6}A peaks into splice junctions

m^{6}A peaks were assigned to the EEJs with reads based on previously described EEJs mapping results. The number of m^{6}A peaks found at exon-exon junctions was determined by overlapping the set of whole m^{6}A peaks to exon-exon junctions. Windows for the junction were generated with their coordinates: 5' 100 nt windows upstream adjacent regions set, 3' 100 nt windows downstream adjacent regions set and 300 nt within these adjacent sites was created. The peaks were translated as single nt point at the center of each peak. BEDTools' intersectBed

was used to count the number of peaks that fell into each window.

M^{6}A-SRSF1/2 related exon splicing

EEJs formed by inclusion of the exon (i.e. a constitutive upstream exon [C1] joined to an alternative cassette exon [A] and an [A] exon joined to a constitutive downstream exon [C2]), referred to as C1A and AC2 junctions, and junction formed by exclusion of the exon (C1C2) were used to identify cassette alternative exons. The inclusion level of a cassette alternative exon was defined as the percentage of exon spliced in (PSI=(C1_A+A_C2)/ (C1_A+A_C2+2*C1_C2)). If the PSI change is over 0.15 between control and FTO-depleted 3T3-L1 cells, these alternative exon was selected as cassette exon. Furthermore, to recognize m^{6}A influencing SRSF2 binding ability variation-induced cassette exons, only cassette exon or their upstream, downstream exons with increased m^{6}A level (FTO-depleted sample compared to control) and with SRSF2 binding sites were selected.

Hierarchical cluster analysis

Gene or isoform lists were used to perform hierarchical cluster analysis by constructing heatmaps using the Gene Cluster 3.0 (http://www.falw.vu/~huik/cluster.htm) and Tree view software.

Gene Ontology

Gene ontology (GO) analysis for specific genes was performed using the DAVID bioinformatics database (http://david.abcc.ncifcrf.gov/) with default parameters [22, 23]. GO classification for the biological process category was performed at default settings. Enriched GO terms with p value less than 0.05 were determined to be statistically significant. Enrichment map of specific genes was constructed by Cytoscape 2.8.3 installed with the Enrichment Map plugin and the parameter is that: $p < 0.001$, FDR $q < 0.1$, overlap cutoff > 0.5 [24].

Statistical analysis

All bioinformatic-associated statistical analyses (unless stated otherwise) were performed using the R software. The t-test using two-way ANOVA in Grouped Analyses of Prism5 software was applied for experimental results (unless stated otherwise).

PAR-CLIP

PAR-CLIP assay was performed as previously described with some minor modifications [25-27]. 3T3-L1 cells were co-transfected pCS2-SR plasmids with control siRNAs, FTO siRNAs or METTL3 siRNAs, respectively. 32 hours later, cells were labeled with 200μM 4-SU (Sigma T4509) for 16 hours, then applied for crosslinking with 0.4 J/cm^2 of 365nm UV light in a crosslinker BLX-E365 (Vilber). Irradiated cells were lysed with NP-40 lysis buffer (50mM pH 7.5 Tris-Cl, 150mM NaCl, 2mM EDTA, 0.5% (v/v) NP40) on ice for 30minutes. Cell debris was removed by centrifugation. The supernatant lysate was digested with RNase T1 (EN0541, Fermentas) in a final concentration of 1U/μl for 15 min at 22℃. Then they lysate was incubated with Flag M2 Affinity Gel (A2220, Sigma) for 2 hours at 4℃. After immunoprecipitation, protein-RNA complex was digested with RNase T1 for the second time in a final concentration of 10U/μl for 20 min at 22℃, then treated with CIP (NEB M0290) in a

final concentration of 0.5U/μl for 10min at 37℃. Then they were subjected to the biotin labelling, following the instruction of RNA 3' end biotinylation kit (20160, Thermo) for further detection. After running on 4%-12% NuPAGE gel (NP0321B0X, Invitrogen), the protein-RNA complexes were transferred to PVDF membrane. Biotin-labelled RNA were detected and visualized following the instruction of the chemiluminescent nuclei acid kit (89880, Thermo). SR proteins were recognized with rabbit Flag antibody (F7425, Sigma).

M^{6}A –RT-qPCR and PAR-CLIP –RT-qPCR

For m^{6}A–RT-qPCR, mRNAs were firstly randomly fragmented into approximately 200nt pieces to facilitate PCR verification. Then it was performed as described in m^{6}A-seq assay but without generation cDNA library. For PAR-CLIP, we partially fragmented RNA with 1U/ul RNase T1 digestion (1x20min), other steps were as described above. Primers were designed within the predicated m^{6}A peaks (around 100 nt) with average PCR product length of 100 bp. We used the same primers to detect both m^{6}A sites and PAR-CLIP binding sites, because the candidate genes we chose have spatially overlapping m6A sites and protein binding sites. For comparing m^{6}A abundance changes and SRSF2 binding ability changes, relative enrichment was first normalized with inputs, and then analyzed by comparing the data from the m^{6}A-immunoprecipitated sample and PAR-CLIP sample respectively. All samples were analyzed in triplicate qPCR. The primer pairs used for m^{6}A-qPCR and PAR-CLIP -qPCR were for GKAP1 (forward): 5'-TCTGTCTCCACTCTTGCCAG-3', GKAP1 (reverse): 5'-TCCCCAGAAATCCTCCCATT-3'. ZFP809 (forward): 5'-TCTGAGTGACACCAGCAAGA-3', ZFP809 (reverse): 5'-CACTTGGTGTCTTTTGGTTAGT-3'. FBXO9 (forward): 5'-CCAGTTCCTGTCGTCCTTTG-3', FBXO9 (reverse): 5'-CCAGGTGTAGGCTCCAGTC-3'. KIF13A (forward): 5'-TCCTCAGCTTCTCTTCCCAC-3', KIF13A (reverse): 5'-CCCCGAGCTAAAGGAGAAG-3'. ZFP212 (forward): 5'-CTCTTGGAATCAGGCCCTG-3', ZFP212 (reverse): 5'-TGAGACTTCTGTTTTCGGGGA-3'. RUNX1T1 exon5 (forward): 5'-CAGCGTGAACTCCTCCACTG-3', RUNX1T1 exon5 (reverse): 5'-CGAGATGTTTCCACTCTTCTG-3'. RUNX1T1 exon6 (forward): 5'-CCAGCGGTACAGTCCAAATAA-3', RUNX1T1 exon6 (reverse): 5'-ATGGCCATATCATCCAATCG-3'. RUNX1T1 exon7 (forward): 5'-ACATGGCACACGTCAAGAAG-3', RUNX1T1 exon7 (reverse): 5'-CGAGATGTTTCCACTCTTCTG -3'.

Supplemental References

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